CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/758,033

CRF Processing Date: 2/13/97
Edited by: _____
Verified by: _____ (STIC staff)

ɕ3

- [ ] Changed a file from non-ASCII to ASCII

- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically: _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____.

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included: _____

- [ ] Deleted extra, invalid, headings used by an applicant, specifically: _____

- [✓] Deleted: [✓] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as_____ .

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically: _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically: _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- [ ] Other: _____
  _____
  _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

TEAM 8

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/758,033*

DATE: 02/13/97
TIME: 12:00:08

INPUT SET: S15493.raw

> This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

```
 1                          SEQUENCE LISTING
 2
 3   (1)      General Information:
 4
 5        (i) APPLICANT: Clayman, Gary L.
 6
 7       (ii) TITLE OF INVENTION: Methods and Compositions for the
 8                Diagnosis and Treatment of Cancer
 9
10      (iii) NUMBER OF SEQUENCES: 14
11
12       (iv) CORRESPONDENCE ADDRESS:
13            (A) ADDRESSEE: Arnold, White and Durkee
14            (B) STREET: P.O. Box 4433
15            (C) CITY: Houston
16            (D) STATE: TX
17            (E) COUNTRY: USA
18            (F) ZIP: 77210-4433
19
20        (v) COMPUTER READABLE FORM:
21            (A) MEDIUM TYPE: Floppy disk
22            (B) COMPUTER: IBM PC compatible
23            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26       (vi) CURRENT APPLICATION DATA:
27            (A) APPLICATION NUMBER:  UNKNOWN
28            (B) FILING DATE: CONCURRENTLY HEREWITH
29            (C) CLASSIFICATION: UNKNOWN
30
31     (viii) ATTORNEY/AGENT INFORMATION:
32            (A) NAME: Highlander, Steven L.
33            (B) REGISTRATION NUMBER: 37,642
34            (C) REFERENCE/DOCKET NUMBER: INGN:022
35
36       (ix) TELECOMMUNICATION INFORMATION:
37            (A) TELEPHONE: (512) 418-3000
38            (B) TELEFAX: (512) 474-7577
39
40
```

--> oK 27

--> oK 29

ERRORED SEQUENCES FOLLOW:

```
456    (2) INFORMATION FOR SEQ ID NO:14:
457
458        (i) SEQUENCE CHARACTERISTICS:
459            (A) LENGTH: 20 base pairs
460            (B) TYPE: nucleic acid
461            (C) STRANDEDNESS: single
462            (D) TOPOLOGY: linear
463
464        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
465
466    TGATTTTGGA GGGATCTCGC                                    20
467
468    A: 85704(1%4_01!.DOC)        delete
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/758,033

INPUT SET: S15493.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: UNKNOWN
29	Wrong Classification	(C) CLASSIFICATION: UNKNOWN
459	Entered (20) and Calc. Seq. Length (21) differ	(A) LENGTH: 20 base pairs
468	Wrong Nucleic Acid Designator	A: 85704(1%4_01!.DOC)
468	# of Sequences for line conflicts w/ running total	A: 85704(1%4_01!.DOC)